#3

OIPE

RAW SEQUENCE LISTING   DATE: 05/16/2002
PATENT APPLICATION: US/10/083,825   TIME: 14:14:06

        Input Set : N:\Crf3\RULE60\10083825.raw
        Output Set: N:\CRF3\05162002\J083825.raw

        SEQUENCE LISTING
 3 (1) GENERAL INFORMATION:
 5   (i) APPLICANT: KHOURI, ROGER K.
 6   SAMPATH, KUBER T.
 7   RUEGER, DAVID C.
 9   (ii) TITLE OF INVENTION: MANUFACTURE OF AUTOGENOUS REPLACEMENT
10   BODY PARTS
12   (iii) NUMBER OF SEQUENCES: 3
14   (iv) CORRESPONDENCE ADDRESS:
15   (A) ADDRESSEE: TESTA, HURWITZ & THIBEAULT
16   (B) STREET: 53 STATE STREET
17   (C) CITY: BOSTON
18   (D) STATE: MASSACHUSETTS   ENTERED
19   (E) COUNTRY: U.S.A.
20   (F) ZIP: 02109
22   (v) COMPUTER READABLE FORM:
23   (A) MEDIUM TYPE: Floppy disk
24   (B) COMPUTER: IBM PC compatible
25   (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26   (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
28   (vi) CURRENT APPLICATION DATA:
C--> 29   (A) APPLICATION NUMBER: US/10/083,825
C--> 30   (B) FILING DATE: 27-Feb-2002
31   (C) CLASSIFICATION:
33   (vii) PRIOR APPLICATION DATA:
34   (A) APPLICATION NUMBER: 08/459,129
35   (B) FILING DATE:
37   (viii) ATTORNEY/AGENT INFORMATION:
38   (A) NAME: KELLEY, ROBIN D.
39   (B) REGISTRATION NUMBER: 34,637
40   (C) REFERENCE/DOCKET NUMBER: CRP-101
42   (ix) TELECOMMUNICATION INFORMATION:
43   (A) TELEPHONE: 617/248-7000
44   (B) TELEFAX: 617/248-7100
47 (2) INFORMATION FOR SEQ ID NO: 1:
49   (i) SEQUENCE CHARACTERISTICS:
50   (A) LENGTH: 1822 base pairs
51   (B) TYPE: nucleic acid
52   (C) STRANDEDNESS: single
53   (D) TOPOLOGY: linear
55   (ii) MOLECULE TYPE: cDNA
57   (iii) HYPOTHETICAL: NO
59   (iv) ANTI-SENSE: NO

RAW SEQUENCE LISTING DATE: 05/16/2002
PATENT APPLICATION: US/10/083,825 TIME: 14:14:06

Input Set : **N:\Crf3\RULE60\10083825.raw**
Output Set: **N:\CRF3\05162002\J083825.raw**

```
61      (vi) ORIGINAL SOURCE:
62           (A) ORGANISM: HOMO SAPIENS
63           (F) TISSUE TYPE: HIPPOCAMPUS
65      (ix) FEATURE:
.66          (A) NAME/KEY: CDS
67           (B) LOCATION: 49..1341
68         · (C) IDENTIFICATION METHOD: experimental
69           (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
70 /product= "OP1"
71 /evidence= EXPERIMENTAL
72 /standard_name= "OP1"
75      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
77 GGTGCGGGCC CGGAGCCCGG AGCCCGGGTA GCGCGTAGAG CCGGCGCG ATG CAC GTG        57
78                                                       Met His Val
79                                                        1
81 CGC TCA CTG CGA GCT GCG GCG CCG CAC AGC TTC GTG GCG CTC TGG GCA        105
82 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
83      5                   10                  15
85 CCC CTG TTC CTG CTG CGC TCC GCC CTG GCC GAC TTC AGC CTG GAC AAC        153
86 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
87 20                  25                  30                  35
89 GAG GTG CAC TCG AGC TTC ATC CAC CGG CGC CTC CGC AGC CAG GAG CGG        201
90 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
91                  40                  45                  50
93 CGG GAG ATG CAG CGC GAG ATC CTC TCC ATT TTG GGC TTG CCC CAC CGC        249
94 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
95              55                  60                  65
97 CCG CGC CCG CAC CTC CAG GGC AAG CAC AAC TCG GCA CCC ATG TTC ATG        297
98 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
99          70                  75                  80
101 CTG GAC CTG TAC AAC GCC ATG GCG GTG GAG GAG GGC GGC GGG CCC GGC       345
102 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
103      85                  90                  95
105 GGC CAG GGC TTC TCC TAC CCC TAC AAG GCC GTC TTC AGT ACC CAG GGC       393
106 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
107 100                 105                 110                 115
109 CCC CCT CTG GCC AGC CTG CAA GAT AGC CAT TTC CTC ACC GAC GCC GAC       441
110 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
111                  120                 125                 130
113 ATG GTC ATG AGC TTC GTC AAC CTC GTG GAA CAT GAC AAG GAA TTC TTC       489
114 Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe
115          ·    135                 140                 145
117 CAC CCA CGC TAC CAC CAT CGA GAG TTC CGG TTT GAT .CTT TCC AAG ATC      537
118 His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile
119          150                 155                 160
121 CCA GAA GGG GAA GCT GTC ACG GCA GCC GAA TTC CGG ATC TAC AAG GAC       585
122 Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp
123      165                 170                 175
125 TAC ATC CGG GAA CGC TTC GAC AAT GAG ACG TTC CGG ATC AGC GTT TAT       633
```

RAW SEQUENCE LISTING   DATE: 05/16/2002
PATENT APPLICATION: US/10/083,825   TIME: 14:14:06

Input Set : N:\Crf3\RULE60\10083825.raw
Output Set: N:\CRF3\05162002\J083825.raw

```
126 Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr
127 180               185           190           195
129 CAG GTG CTC CAG GAG CAC TTG GGC AGG GAA TCG GAT CTC TTC CTG CTC      681
130 Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu
131               200           205           210
133 GAC AGC CGT ACC CTC TGG GCC TCG GAG GAG GGC TGG CTG GTG TTT GAC      729
134 Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp
135               215           220           225
137 ATC ACA GCC ACC AGC AAC CAC TGG GTG GTC AAT CCG CGG CAC AAC CTG      777
138 Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu
139               230           235           240
141 GGC CTG CAG CTC TCG GTG GAG ACG CTG GAT GGG CAG AGC ATC AAC CCC      825
142 Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro
143       245               250           255
145 AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC      873
146 Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro
147 260               265           270           275
149 TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC      921
150 Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile
151               280           285           290
153 CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG CCC      969
154 Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro
155               295           300           305
157 AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC      1017
158 Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser
159               310           315           320
161 AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC      1065
162 Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
163       325               330           335
165 CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC      1113
166 Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala
167 340               345           350           355
169 GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG      1161
170 Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met
171               360           365           370
173 AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC      1209
174 Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn
175               375           380           385
177 CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC      1257
178 Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala
179               390           395           400
181 ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA      1305
182 Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys
183       405               410           415
185 TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC           1351
186 Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
187 420               425           430
189 GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG    1411
191 GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG    1471
```

```
193 TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC   1531
195 ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC   1591
197 GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT   1651
199 CGTTTCCAGA GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG   1711
201 GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC   1771
203 CTGTAATAAA TGTCACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAA A              1822
```

206 (2) INFORMATION FOR SEQ ID NO: 2:
208   (i) SEQUENCE CHARACTERISTICS:
209   (A) LENGTH: 431 amino acids
210   (B) TYPE: amino acid
211   (D) TOPOLOGY: linear
213   (ii) MOLECULE TYPE: protein
215   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
217 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
218  1               5                  10                 15
220 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
221              20                  25                 30
223 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
224          35                  40                 45
226 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
227      50                  55                 60
229 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
230  65                  70                 75                 80
232 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
233              85                  90                 95
235 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
236              100                 105                110
238 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
239          115                 120                 125
241 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
242      130                 135                 140
244 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
245 145                 150                 155                160
247 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
248              165                 170                175
250 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
251          180                 185                 190
253 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
254          195                 200                 205
256 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
257      210                 215                 220
259 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
260 225                 230                 235                240
262 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
263              245                 250                255
265 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
266          260                 265                 270
268 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
269          275                 280                 285
```

```
271 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
272     290             295             300
274 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
275 305             310             315             320
277 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
278             325             330             335
280 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
281         340             345             350
283 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
284         355             360             365
286 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
287     370             375             380
289 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
290 385             390             395             400
292 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
293             405             410             415
295 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
296         420             425             430
299 (2) INFORMATION FOR SEQ ID NO: 3:
301     (i) SEQUENCE CHARACTERISTICS:
302         (A) LENGTH: 102 amino acids
303         (B) TYPE: amino acid
304         (D) TOPOLOGY: linear
306     (ii) MOLECULE TYPE: protein
309     (ix) FEATURE:
310         (A) NAME/KEY: Protein
311         (B) LOCATION: 1..102
312         (D) OTHER INFORMATION: /label= OPX
313 /note= "WHEREIN EACH XAA IS INDEPENDENTLY SELECTED
314 FROM A GROUP OF ONE OR MORE SPECIFIED AMINO ACIDS
315 AS DEFINED IN THE SPECIFICATION"
318     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
W--> 320     Cys Xaa Xaa His Glu Leu Tyr Val Xaa Phe Xaa Asp Leu Gly Trp Xaa
321     1             5             10             15
W--> 323     Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
324             20             25             30
W--> 326     Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
327             35             40             45
W--> 329     Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
330         50             55             60
W--> 332     Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
333     65             70             75             80
W--> 335     Asp Xaa Ser Xaa Asn Val Xaa Leu Xaa Lys Xaa Arg Asn Met Val Val
336             85             90             95
W--> 338     Xaa Ala Cys Gly Cys His
339             100
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/16/2002
PATENT APPLICATION: US/10/083,825   TIME: 14:14:07

Input Set : N:\Crf3\RULE60\10083825.raw
Output Set: N:\CRF3\05162002\J083825.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos.2,3,9,11,16,19,23,26,35,39,41,50,52,56,57,58,60,61,65,71,73
Seq#:3; Xaa Pos.75,80,82,84,87,89,91,97

VERIFICATION SUMMARY   DATE: 05/16/2002
PATENT APPLICATION: US/10/083,825   TIME: 14:14:07

Input Set : **N:\Crf3\RULE60\10083825.raw**
Output Set: **N:\CRF3\05162002\J083825.raw**

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:320 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:16
L:326 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:32
L:329 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:48
L:332 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:64
L:335 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:80
L:338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:96